

L Number	Hits	Search Text	DB	Time stamp
1	3	penner-reinhold.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:25
2	2	fleig-andrea.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:25
3	10	ltrpc2	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:26
4	1	wo adj "200029571"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:51
5	1	wo adj "200040614"	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:27
6	2	6548272.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/06/29 15:51

10007706 Results:

SEQ ID NO: 1

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	7950	100.0	1503	3	AA92944	Aay92944 Human TRP
2	7950	100.0	1503	3	AA95439	Aay95439 Human cal
3	7950	100.0	1503	3	AB36865	Aab36865 Human put
4	7950	100.0	1503	5	AB76459	Abb76459 Human lon
5	7950	100.0	1503	5	AB84544	Abb84544 Human tra
6	7950	100.0	1503	7	ADC47022	Adc47022 Human LTR
7	7950	100.0	1503	7	ADC77685	Adc77685 Human 222
8	7950	100.0	1503	7	ADC83633	Adc83633 LTRPC3-re
9	7741	97.4	1469	6	AB43185	Abr43185 Human REM
10	6740.5	84.8	1508	7	ADC47024	Adc47024 Rat LTRPC
11	6709	84.4	1507	7	ADC47034	Adc47034 Mouse LTR
12	2771	34.9	525	6	ADA56830	Ada56830 Human sec
13	2771	34.9	525	6	AB47695	Abr47695 Human sec
14	2771	34.9	525	6	ABR00046	Abr00046 Human gen
15	2771	34.9	525	7	ADB91501	Adb91501 Human sec
16	2771	34.9	525	7	ADC74074	Adc74074 Human sec

RESULT 1

AA92944

ID AA92944 standard; protein; 1503 AA.

XX

AC AA92944;

XX

DT 08-NOV-2000 (first entry)

XX

DE Human TRPC7 protein.

XX

KW Transmembrane protein; TRPC7; brain; transient receptor potential; TRP;

KW calcium channel function; human; gene therapy; periodic psychosis;

KW mutation.

XX

OS Homo sapiens.

XX

PN WO200029571-A1.

XX

PD 25-MAY-2000.

XX

PF 11-NOV-1999; 99WO-JP006289.

XX

PR 12-NOV-1998; 98JP-00321200.

XX

PA (EIKE) EIKEN KAGAKU KK.

XX

PI Shimizu N, Nagamine K;

XX

DR WPI; 2000-387784/33.

DR

N-PSDB; AAA11284.

XX

PT Nucleic acids encoding transmembrane protein TRPC7 expressed in brain and

PT homologous to transient receptor potential protein useful in the of

PT treatment of associated diseases such as periodic psychosis.

XX

PS Claim 1; Page 64-71; 77pp; Japanese.

XX

CC The invention relates to the isolation of a nucleic acid encoding a
 CC transmembrane protein TRPC7 which is expressed in brain and is homologous
 CC to transient receptor potential (TRP) protein. This suggests that the
 CC TRPC7 protein may have a calcium channel function. This sequence
 CC represents the human TRPC7 protein. The DNA and protein can be used in
 CC the diagnosis and treatment of disorders associated with TRPC7,

CC especially the screening, monitoring and treatment (by gene therapy) of
CC periodic psychosis, which appears to be associated with mutations in the
CC TRPC7 gene
XX
SQ Sequence 1503 AA;

Query Match 100.0%; Score 7950; DB 3; Length 1503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSALRKAGSEQEEGFEGLP RRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
      |||
Db      1 MEPSALRKAGSEQEEGFEGLP RRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60

Qy     61 SWIPENIKKKECVYFVESSKLS DAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120
      |||
Db     61 SWIPENIKKKECVYFVESSKLS DAGKVVCQCGYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120

Qy    121 EMPTDAFGDIVFTGLSQVKVYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180
      |||
Db    121 EMPTDAFGDIVFTGLSQVKVYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180

Qy    181 NMKPRLKSIFRRGLVKVAQTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240
      |||
Db    181 NMKPRLKSIFRRGLVKVAQTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240

Qy    241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSFILVDDGTHGQYGEVIP 300
      |||
Db    241 VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSFILVDDGTHGQYGEVIP 300

Qy    301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATNGTPCVVVEGSGRVA 360
      |||
Db    301 LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATNGTPCVVVEGSGRVA 360

Qy    361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420
      |||
Db    361 DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR 420

Qy    421 EGKDGQDDVDVAILQALLKASRSQDHFHGHENWDHQLKLAVAWNVRVDIARSEIFMDEWQWK 480
      |||
Db    421 EGKDGQDDVDVAILQALLKASRSQDHFHGHENWDHQLKLAVAWNVRVDIARSEIFMDEWQWK 480

Qy    481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540
      |||
Db    481 PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL 540

Qy    541 VEDPERPACAPAPRLQMHHVAQVLRRELLGDFTPQLYPRPRHNDRLRLLLVPVPHVKLNQV 600
      |||
Db    541 VEDPERPACAPAPRLQMHHVAQVLRRELLGDFTPQLYPRPRHNDRLRLLLVPVPHVKLNQV 600

Qy    601 GVSLSRLYKRSSGHVFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660
      |||
Db    601 GVSLSRLYKRSSGHVFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK 660

Qy    661 ELSKEEEDTSSEMLALAEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720
      |||
Db    661 ELSKEEEDTSSEMLALAEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL 720

Qy    721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCLMAFPLLLTGLISFREKRLQD 780
      |||
Db    721 ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCLMAFPLLLTGLISFREKRLQD 780

Qy    781 VGTPAARARAFFTAPVVVFHLNLSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFLSLV 840
      |||
Db    781 VGTPAARARAFFTAPVVVFHLNLSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFLSLV 840

Qy    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900
      |||
Db    841 CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS 900

Qy    901 LDFILFCLRLMHIFTISKTLGPKIIIVKRMMDVFFFLFLLAVVVVSFGVAKQAILIHNE 960
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Db	901	LDLFI L FCLRLMHIFTISKTLGPKIIIVKRMMDVFFFLFLAVVVSFGVAKQAILIHNE	960
Qy	961	RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF	1020
Db	961	RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF	1020
Qy	1021	PEWLTVLLCLLYLLFTNILLNLLIAMFNNTFQQVQEHTDQIWKQRHDLIEEYHGRPAA	1080
Db	1021	PEWLTVLLCLLYLLFTNILLNLLIAMFNNTFQQVQEHTDQIWKQRHDLIEEYHGRPAA	1080
Qy	1081	PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLNQRQFQQ	1140
Db	1081	PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLNQRQFQQ	1140
Qy	1141	KQRPEQKIEDISNKVDAMVDLLDLPLKRSMSMEQRLASLEEQVAQTARALHWIVRTLRA	1200
Db	1141	KQRPEQKIEDISNKVDAMVDLLDLPLKRSMSMEQRLASLEEQVAQTARALHWIVRTLRA	1200
Qy	1201	SGFSSEADVPTLASQKAAEEDPAEPGGRKKTEEPGDSYHVNRHLLYPNCPVTRFPVPNE	1260
Db	1201	SGFSSEADVPTLASQKAAEEDPAEPGGRKKTEEPGDSYHVNRHLLYPNCPVTRFPVPNE	1260
Qy	1261	KVPWETEFLLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ	1320
Db	1261	KVPWETEFLLIYDPPFYTAERKDAAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ	1320
Qy	1321	AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNEDGAICRKSIIKKMLEVLVVKLP	1380
Db	1321	AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNEDGAICRKSIIKKMLEVLVVKLP	1380
Qy	1381	LSEHWALPGGSREPGEMLPRLKRLRQEHWPSEFENLLKCGMEVYKGYMDDPRNTDPAWI	1440
Db	1381	LSEHWALPGGSREPGEMLPRLKRLRQEHWPSEFENLLKCGMEVYKGYMDDPRNTDPAWI	1440
Qy	1441	ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRIPLYANHKTLQKAAAEFG	1500
Db	1441	ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRIPLYANHKTLQKAAAEFG	1500
Qy	1501	AHY 1503	
Db	1501	AHY 1503	

RESULT 2

AA95439

ID AA95439 standard; protein; 1503 AA.

XX

AC AA95439;

XX

DT 10-OCT-2000 (first entry)

XX

DE Human calcium channel polypeptide.

XX

KW Human; SOC-2/CRAC-1; calcium channel; store operated channel;

KW calcium release activated channel; therapy; diagnosis;

KW lymphocyte proliferative disorder.

XX

OS Homo sapiens.

XX

PN WO200040614-A2.

XX

PD 13-JUL-2000.

XX

PF 20-DEC-1999; 99WO-US029996.

XX

PR 30-DEC-1998; 98US-0114220P.

PR 29-JAN-1999; 99US-0120018P.

PR 22-JUN-1999; 99US-0140415P.

XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Scharenberg AM;
 XX
 DR WPI; 2000-465957/40.
 DR N-PSDB; AAA49926.
 XX
 PT New SOC/CRAC calcium channel polynucleotides and polypeptides used to
 PT diagnose and treat proliferative disorders associated with the channel,
 PT and to screen for novel modulators of the channel.
 XX
 PS Example; Page 69-72; 108pp; English.
 XX
 CC The present sequence is that of a human calcium channel polypeptide as
 CC deduced from a cDNA clone (see AAA49926) identified in an EST database
 CC search for sequences showing homology to *Caenorhabditis elegans* calcium
 CC signal sequences. Clones isolated from such screenings were used to
 CC identify human clones (see AAA49922-24) encoding members (see AAY95435-
 CC 37) of a new family of SOC (store operated channel) or CRAC (calcium
 CC release activated channel) calcium channel polypeptides. SOC/CRAC
 CC polypeptides modulate Ca²⁺ flux into and out of a cell, and may be
 CC activated upon depletion of Ca²⁺ from intracellular calcium stores,
 CC allowing Ca²⁺ influx into a cell. SOC/CRAC polypeptides and
 CC polynucleotides can be used to treat patients that require modulation of
 CC calcium influx into their SOC/CRAC-expressing cells. Polypeptides can be
 CC used to deliver therapeutic and/or imaging agents to such cells to
 CC modulate proliferation and growth. SOC/CRAC polypeptides also represent
 CC targets for designing and/or identifying inhibitors that block lymphocyte
 CC proliferation and binding agents that selectively bind to SOC/CRAC
 CC polypeptides to which drugs or toxins can be conjugated for delivery to
 CC SOC/CRAC expressing cells
 XX
 SQ Sequence 1503 AA;

Query Match 100.0%; Score 7950; DB 3; Length 1503;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEPSALRKAGSEQEEGFEGLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60

RESULT 3

AAB36865

ID AAB36865 standard; protein; 1503 AA.
 XX
 AC AAB36865;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE Human putative Ca²⁺ channel protein TrpC7 protein.
 XX
 KW mutTCCCH-1; sugar-phosphate hydrolase; NUDT9.
 XX
 OS Homo sapiens.
 XX
 PN WO200065056-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-US011319.
 XX
 PR 26-APR-1999; 99US-0131051P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Scharenberg AM;
 XX
 DR WPI; 2000-687347/67.

DR N-PSDB; AAC68399.
XX
PT Novel nucleic acids encoding a MutT domain-containing polypeptide present
PT in human calcium channel protein TrpC7, useful for diagnostic and
PT therapeutic purposes.
XX
PS Claim 39; Page 65; 69pp; English.
XX
CC The present invention relates to human mutTCCH-1. Therapeutics involving
CC mutTCCH-1 may be useful for diagnosing and treating conditions associated
CC with aberrant levels of expression of (II) and for identifying agents
CC that are useful for treating diseases associated with
CC pyrophosphohydrolase and/or sugar-phosphate hydrolase activity
XX
SQ Sequence 1503 AA;

Query Match 100.0%; Score 7950; DB 3; Length 1503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSALRKAGSEQEEGFEGLP	RRVTD	LG	MV	SN	LR	RS	NS	SL	FK	SW	R	L	Q	CP	FG	NN	D	K	Q	E	S	L	S	60																											
Db	1	MEPSALRKAGSEQEEGFEGLP	RRVTD	LG	MV	SN	LR	RS	NS	SL	FK	SW	R	L	Q	CP	FG	NN	D	K	Q	E	S	L	S	60																											
Qy	61	SWIPENIKKKECVYFV	ESSK	LS	DAG	KV	VC	QCG	Y	T	H	E	Q	H	L	E	E	A	T	K	P	H	T	F	Q	G	T	Q	W	D	P	K	K	H	V	Q	120																
Db	61	SWIPENIKKKECVYFV	ESSK	LS	DAG	KV	VC	QCG	Y	T	H	E	Q	H	L	E	E	A	T	K	P	H	T	F	Q	G	T	Q	W	D	P	K	K	H	V	Q	120																
Qy	121	EMPTDAFGDIVFTGL	SQ	KV	KY	V	R	V	S	Q	D	T	P	S	S	V	I	Y	H	L	M	T	Q	H	W	G	L	D	V	P	N	L	L	I	S	V	T	G	G	A	K	N	F	180									
Db	121	EMPTDAFGDIVFTGL	SQ	KV	KY	V	R	V	S	Q	D	T	P	S	S	V	I	Y	H	L	M	T	Q	H	W	G	L	D	V	P	N	L	L	I	S	V	T	G	G	A	K	N	F	180									
Qy	181	NMKPRLKSIFRRGL	V	K	V	A	Q	T	T	G	A	W	I	T	G	G	S	H	T	G	V	M	K	Q	V	G	E	A	V	R	D	F	S	L	S	S	S	Y	K	E	G	E	L	I	T	I	G	240					
Db	181	NMKPRLKSIFRRGL	V	K	V	A	Q	T	T	G	A	W	I	T	G	G	S	H	T	G	V	M	K	Q	V	G	E	A	V	R	D	F	S	L	S	S	S	Y	K	E	G	E	L	I	T	I	G	240					
Qy	241	VATWGTVHRREGLI	H	P	T	G	S	F	P	A	E	Y	I	L	D	E	D	G	Q	G	N	L	T	C	L	D	S	N	H	S	F	I	L	V	D	D	G	T	H	G	Y	Q	Y	G	V	E	I	P	300				
Db	241	VATWGTVHRREGLI	H	P	T	G	S	F	P	A	E	Y	I	L	D	E	D	G	Q	G	N	L	T	C	L	D	S	N	H	S	F	I	L	V	D	D	G	T	H	G	Y	Q	Y	G	V	E	I	P	300				
Qy	301	LRTLEKFISEQTKE	R	G	G	V	A	I	K	I	P	I	V	C	V	V	L	E	G	G	P	G	T	L	H	T	I	D	N	A	T	T	N	G	T	P	C	V	V	E	G	S	G	R	V	A	360						
Db	301	LRTLEKFISEQTKE	R	G	G	V	A	I	K	I	P	I	V	C	V	V	L	E	G	G	P	G	T	L	H	T	I	D	N	A	T	T	N	G	T	P	C	V	V	E	G	S	G	R	V	A	360						
Qy	361	DVIAQVANLPVSDI	T	I	S	L	I	Q	Q	K	L	S	V	F	F	Q	E	M	F	E	T	F	T	E	S	R	I	V	E	W	T	K	K	I	Q	D	I	V	R	R	R	Q	L	L	T	V	F	R	420				
Db	361	DVIAQVANLPVSDI	T	I	S	L	I	Q	Q	K	L	S	V	F	F	Q	E	M	F	E	T	F	T	E	S	R	I	V	E	W	T	K	K	I	Q	D	I	V	R	R	R	Q	L	L	T	V	F	R	420				
Qy	421	EGKDGQQDQDV	V	A	I	L	Q	A	L	L	K	A	S	R	S	Q	D	H	F	G	H	E	N	W	D	H	Q	L	K	L	A	V	A	W	N	R	V	D	I	A	R	S	E	I	F	M	D	E	W	Q	W	K	480
Db	421	EGKDGQQDQDV	V	A	I	L	Q	A	L	L	K	A	S	R	S	Q	D	H	F	G	H	E	N	W	D	H	Q	L	K	L	A	V	A	W	N	R	V	D	I	A	R	S	E	I	F	M	D	E	W	Q	W	K	480
Qy	481	PSDLHPTMTAALI	S	N	K	P	E	F	V	K	L	F	L	E	N	G	V	Q	L	K	E	F	V	T	W	D	T	L	L	Y	L	Y	E	N	L	D	P	S	C	L	F	H	S	K	L	Q	K	V	L	540			
Db	481	PSDLHPTMTAALI	S	N	K	P	E	F	V	K	L	F	L	E	N	G	V	Q	L	K	E	F	V	T	W	D	T	L	L	Y	L	Y	E	N	L	D	P	S	C	L	F	H	S	K	L	Q	K	V	L	540			
Qy	541	VEDPERPACAPAA	P	R	L	Q	M	H	H	V	A	Q	V	L	R	E	L	G	D	F	T	Q	P	L	Y	P	R	P	R	H	N	D	R	L	R	L	L	L	P	V	P	H	V	K	L	N	V	Q	600				
Db	541	VEDPERPACAPAA	P	R	L	Q	M	H	H	V	A	Q	V	L	R	E	L	G	D	F	T	Q	P	L	Y	P	R	P	R	H	N	D	R	L	R	L	L	L	P	V	P	H	V	K	L	N	V	Q	600				
Qy	601	GVSLRSLYKRSSG	H	V	T	F	T	M	D	P	I	R	D	L	L	I	W	A	I	V	Q	N	R	R	E	L	A	G	I	I	W	A	Q	S	Q	D	C	I	A	A	A	L	A	C	S	K	I	L	K	660			
Db	601	GVSLRSLYKRSSG	H	V	T	F	T	M	D	P	I	R	D	L	L	I	W	A	I	V	Q	N	R	R	E	L	A	G	I	I	W	A	Q	S	Q	D	C	I	A	A	A	L	A	C	S	K	I	L	K	660			
Qy	661	ELSKEEEDTDSSE	E	M	L	A	L	A	E	E	Y	E	H	R	A	I	G	V	F	T	E	C	Y	R	K	D	E	E	R	A	Q	K	L	L	T	R	V	S	E	A	W	G	K	T	T	C	L	Q	L	720			
Db	661	ELSKEEEDTDSSE	E	M	L	A	L	A	E	E	Y	E	H	R	A	I	G	V	F	T	E	C	Y	R	K	D	E	E	R	A	Q	K	L	L	T	R	V	S	E	A	W	G	K	T	T	C	L	Q	L	720			
Qy	721	ALEAKDMKFVSHG	G	I	Q	A	F	L	T	K	V	W	W	Q	L	S	V	D	N	G	L	W	R	V	T	L	C	M	L	A	F	P	L	L	L	T	G	L	I	S	F	R	E	K	R	L	Q	D	780				
Db	721	ALEAKDMKFVSHG	G	I	Q	A	F	L	T	K	V	W	W	Q	L	S	V	D	N	G	L	W	R	V	T	L	C	M	L	A	F	P	L	L	L	T	G	L	I	S	F	R	E	K	R	L	Q	D	780				

Qy	781	VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV	840
Db	781	VGTPAARARAFFTAPVVVFHLNILSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV	840
Qy	841	CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS	900
Db	841	CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS	900
Qy	901	LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVVVVSFGVAKQAILIHNE	960
Db	901	LDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDVFFFLFLLAVVVVSFGVAKQAILIHNE	960
Qy	961	RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF	1020
Db	961	RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF	1020
Qy	1021	PEWLTVLLLCLYLLFTNILLNLLIAMFNITFQQVQEHTDQIWKFORHDLIEYHGRPAA	1080
Db	1021	PEWLTVLLLCLYLLFTNILLNLLIAMFNITFQQVQEHTDQIWKFORHDLIEYHGRPAA	1080
Qy	1081	PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ	1140
Db	1081	PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLQNRQFQQ	1140
Qy	1141	KQRPEQKIEDISNKVDAMVDLLDPLKRSMSMEQRLASLEEQAQTARALHWIVRTLRA	1200
Db	1141	KQRPEQKIEDISNKVDAMVDLLDPLKRSMSMEQRLASLEEQAQTARALHWIVRTLRA	1200
Qy	1201	SGFSSEADVPTLASQKAAEEDAEPPGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE	1260
Db	1201	SGFSSEADVPTLASQKAAEEDAEPPGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE	1260
Qy	1261	KVPWETEFLLIYDPPFYTAERKDAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ	1320
Db	1261	KVPWETEFLLIYDPPFYTAERKDAAMDPMGDTLEPLSTIQYNVVDGLRDRRSFHGPYTVQ	1320
Qy	1321	AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNRNEDGAICRKSIIKMLEVLVVKLP	1380
Db	1321	AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNRNEDGAICRKSIIKMLEVLVVKLP	1380
Qy	1381	LSEHWALPGGSREPGEMLPRLKRLRQEHWPSPFNLLKCGMEVYKGYMDDPRNTDPAWI	1440
Db	1381	LSEHWALPGGSREPGEMLPRLKRLRQEHWPSPFNLLKCGMEVYKGYMDDPRNTDPAWI	1440
Qy	1441	ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRIPLYANHKTLQKAAAEFG	1500
Db	1441	ETVAVSVHFQDQNDVELNRLNSNLHACDSGASIRWQVVDRIPLYANHKTLQKAAAEFG	1500
Qy	1501	AHY	1503
Db	1501	AHY	1503

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	7950	100.0	1503	4	US-09-600-087-2	Sequence 2, Appli
2	2216	27.9	1095	4	US-09-636-215-780	Sequence 780, App
3	2216	27.9	1095	4	US-09-685-166A-780	Sequence 780, App
4	2212	27.8	1095	3	US-09-112-096-15	Sequence 15, Appl
5	2212	27.8	1095	4	US-09-636-215-778	Sequence 778, App
6	2212	27.8	1095	4	US-09-685-166A-778	Sequence 778, App
7	1423	17.9	1533	1	US-08-623-679-9	Sequence 9, Appli
8	1423	17.9	1533	3	US-08-933-774-9	Sequence 9, Appli
9	1423	17.9	1533	3	US-09-181-030-9	Sequence 9, Appli
10	1423	17.9	1533	4	US-09-534-242-9	Sequence 9, Appli
11	1423	17.9	1533	4	US-09-454-854-9	Sequence 9, Appli

12	1423	17.9	1533	4	US-09-164-671-9	Sequence 9, Appli
13	1341	16.9	1497	1	US-08-623-679-7	Sequence 7, Appli
14	1341	16.9	1497	3	US-08-933-774-7	Sequence 7, Appli
15	1341	16.9	1497	3	US-09-181-030-7	Sequence 7, Appli

RESULT 1

US-09-600-087-2

; Sequence 2, Application US/09600087

; Patent No. 6548272

; GENERAL INFORMATION:

; APPLICANT: Shimizu, No. 6548272uyoshi

; APPLICANT: Nagamine, Kentaro

; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN

; FILE REFERENCE: 11283-004001

; CURRENT APPLICATION NUMBER: US/09/600,087

; CURRENT FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: PCT/JP99/06289

; PRIOR FILING DATE: 1999-11-11

; PRIOR APPLICATION NUMBER: JP/321200/1998

; PRIOR FILING DATE: 1998-11-12

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1503

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: TRANSMEM

; LOCATION: (320)...(344)

; NAME/KEY: TRANSMEM

; LOCATION: (750)...(773)

; NAME/KEY: TRANSMEM

; LOCATION: (794)...(818)

; NAME/KEY: TRANSMEM

; LOCATION: (867)...(891)

; NAME/KEY: TRANSMEM

; LOCATION: (900)...(924)

; NAME/KEY: TRANSMEM

; LOCATION: (932)...(956)

; NAME/KEY: TRANSMEM

; LOCATION: (1024)...(1048)

US-09-600-087-2

Query Match 100.0%; Score 7950; DB 4; Length 1503;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSALRKAGSEQEEGFEGFLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS	60
Db	1	MEPSALRKAGSEQEEGFEGFLPRRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS	60
Qy	61	SWIPENIKKKECVYFVESSKLS DAGKVVQCQGYTHEQHLEEATKPHTFQGTQWDPKKHVQ	120
Db	61	SWIPENIKKKECVYFVESSKLS DAGKVVQCQGYTHEQHLEEATKPHTFQGTQWDPKKHVQ	120
Qy	121	EMPTDAFGDIVFTGLSQVKVYVRVSQDTPSSVIYHMTQHWGLDVPNLLISVTGGAKNF	180
Db	121	EMPTDAFGDIVFTGLSQVKVYVRVSQDTPSSVIYHMTQHWGLDVPNLLISVTGGAKNF	180
Qy	181	NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG	240
Db	181	NMKPRLKSIFRRGLVKVAQTTGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG	240
Qy	241	VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVVEIP	300
Db	241	VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGVVEIP	300
Qy	301	LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA	360
Db	301	LRTRLEKFISEQTKERGGVAIKIPIVCVVLEGGPGTLHTIDNATTNGTPCVVVEGSGRVA	360

Qy	361	DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR	420
Db	361	DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR	420
Qy	421	EGKDGQQDQDVAAILQALLKASRSQDHFHGHENWDHQLKLAVAWNVRVDIARSEIFMDEWQWK	480
Db	421	EGKDGQQDQDVAAILQALLKASRSQDHFHGHENWDHQLKLAVAWNVRVDIARSEIFMDEWQWK	480
Qy	481	PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL	540
Db	481	PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL	540
Qy	541	VEDPERPACAPAAPRLQMHHVAQVLRRELLGDFQTPLYPRPRHNDRLRLLLPVPHVKLVNQ	600
Db	541	VEDPERPACAPAAPRLQMHHVAQVLRRELLGDFQTPLYPRPRHNDRLRLLLPVPHVKLVNQ	600
Qy	601	GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK	660
Db	601	GVSLRSLYKRSSGHVTFTMDPIRDLLIWAIVQNRRELAGIIWAQSQDCIAAALACSKILK	660
Qy	661	ELSKEEEDTDSSEMLALAEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL	720
Db	661	ELSKEEEDTDSSEMLALAEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL	720
Qy	721	ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCLMAFPLLLTGLISFREKRLQD	780
Db	721	ALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCLMAFPLLLTGLISFREKRLQD	780
Qy	781	VGTPAARARAFFTAPVVVFHLNLSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV	840
Db	781	VGTPAARARAFFTAPVVVFHLNLSYFAFLCLFAYVLMVDFQPVPSWCECAIYLWLFSLV	840
Qy	841	CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS	900
Db	841	CEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILLFVAGLTCRLIPATLYPGRVILS	900
Qy	901	LDFILFCLRLMHIFTISKTLGPKIIIVKRMKDVFFFLFLLAVVWVSFGVAKQAILIHNE	960
Db	901	LDFILFCLRLMHIFTISKTLGPKIIIVKRMKDVFFFLFLLAVVWVSFGVAKQAILIHNE	960
Qy	961	RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF	1020
Db	961	RRVDWLFRGAVYHSYLTIFGQIPGYIDGVNFNPEHCSPNGTDPYKPKCPESDATQQRPAF	1020
Qy	1021	PEWLTVLLLCLYLLFTNILLNLLIAMFNFTFQQVQEHTDQIWKFORHDLIEEYHGRPAA	1080
Db	1021	PEWLTVLLLCLYLLFTNILLNLLIAMFNFTFQQVQEHTDQIWKFORHDLIEEYHGRPAA	1080
Qy	1081	PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLNQRQFQQ	1140
Db	1081	PPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEKNEEAALLSWEIYLKENYLNQRQFQQ	1140
Qy	1141	KQRPEQKIEDISNKVDAMVDLLDLPLKRSGSMEQRLASLEEQAQTARALHWIVRTLRA	1200
Db	1141	KQRPEQKIEDISNKVDAMVDLLDLPLKRSGSMEQRLASLEEQAQTARALHWIVRTLRA	1200
Qy	1201	SGFSSEADVPTLASQKAAEPPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE	1260
Db	1201	SGFSSEADVPTLASQKAAEPPDAEPGGRKKTEEPGDSYHVNARHLLYPNCPVTRFPVPNE	1260
Qy	1261	KVPWETEFLIYDPPFYTAERKDAAMDPMDTLEPLSTIQYNVVDGLDRRSFHGPYTVQ	1320
Db	1261	KVPWETEFLIYDPPFYTAERKDAAMDPMDTLEPLSTIQYNVVDGLDRRSFHGPYTVQ	1320
Qy	1321	AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNEDGAICRKSIIKMLEVLVVKLP	1380
Db	1321	AGLPLNPMGRTGLRGRGSLSCFGPNHTLYPMVTRWRNEDGAICRKSIIKMLEVLVVKLP	1380
Qy	1381	LSEHWALPGGSREPGEMLPRLKRLRQEHWPSEFNLLKCGMEVYKGYMDDPRNTDNAWI	1440

Db 254 VDNGCHGHPTVEAKLRNQLEKYISERTIQDSNYGGKIPIVCFAQGGGKETLKAINTSIKN 313

Qy 347 GTPCVVVEGSGRVADVIAQVANLPVSD-ITISLIQOKLSVFFQEMFETFTESRIVEWTKK 405

Db 314 KIPCVVVEGSGQIADVIASL--VEVEDALTSSAVKEKLVRFPLRTVSRLPBEETESWIKW 371

Qy 406 IQDIVRRRQLLTVFREGKDGQDQVDVAILQALLKASRSQDHFHGHENWDHQLKLAVAWNRV 465

Db 372 LKEILECSHLLTVIKMEEAGDEIVSN AISYALYKAFSTSEQ-DKDNWNGQLKLLLEWNQL 430

Qy 466 DIARSEIFMDEWQWKPSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLLYEN 525

Db 431 DIANDEIFTNDRRWESADLQEVMTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFNSN 490

Qy 526 LDPSCLFHSKQLKVLVEDPERPACAPAAPRLQMHHVAQVLRRELLGDFQTPLYPRPRHNR 585

Db 491 -HFSTLVYRNQLQ-----IAKNSYNDALLTFVWKL VANFRGRGFRKEDR-NGR 534

Qy 586 LRLLLPVPHVKLVNQGVSLRSLYKRSSGHVTFMDPIRDLLIWAIVQNRRELAGIWAQS 645

Db 535 -----DEMDIELHDVS-----PITRHLPLQALFIWAILQNKKELSKVIEQT 575

Qy 646 QDCIAAALACSKILKELSKEEEDTDSSEMLALAEYEHRAIGVFTECYRKDEERAQKLL 705

Db 576 RGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDLAEQLL 635

Qy 706 TRVSEAWGKTTCLQLALEAKDMKFVSHGGIQAFLTKVWWGQLSVDNGLWRVTLCLMAFPL 765

Db 636 VYSCEAWGGSNCLELAVEATDQHFIAPGVQNFSLKQWYGEISRDTKNWKIILCLFIPL 695

Qy 766 LLTGLISFREKRLQDVGTPAARAR-----AFFTAPVVVFHNLISYFAFLCLFAYVLM 818

Db 696 VGCGFVSFRKK-----PVDKHKLLWYYVAFFTSFVVFVSWNVVFYIAFLLLFAYVLL 748

Qy 819 VDFQPVPWSWCECAIYLWLFSLVCEEMRQLFYDPDECGLMKKAALYFSDFWNKLDVGAILL 878

Db 749 MDFHSPVHPPELVLYSLVFLFCDEVQRQWYV-----GVNYFTDLWNVMDTLGLFY 799

Qy 879 FVAGLTCLRL--IPATLYPGRVILSLDFILFCLRLMHIFTISKTLGPKIIIVKRMMKDV 935

Db 800 FIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTVSRNLGPKIIMLQRLIDVF 859

Qy 936 FFLFLLAVWVVSFGVAKQAILIHNERRVDWLFGRGAVYHSYLTIFGQIPGYIDGVNFNPEH 995

Db 860 FFLFLFAXWMVAFGVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDVGTTYDFAH 919

Qy 996 CSPNGTDPYKPKCPESDATQQRPAFPEWLTVLLCLYLLFTNILLNLLIAMFNNTFQQV 1055

Db 920 CTFTGNES-KPLCVELD-EHNLPRFPEWITPLVCIYMLSTNILLVNLVAMFGYTVGT 977

Qy 1056 QEHTDQIWKFORHDLIEEYHGRPAAPPPFILLSHLQLFIKRVVLKTPAKRHKQLKNKLEK 1115

Db 978 QENNDQVWKQRYFLVQEYCSRLNIPFPFIVFAYFYMVKKCFKCCCKEKNMESSVCCPK 1037

Qy 1116 NEEAALLSWEIYLKENYLQNRQFQQKQRPQK-----IEDISNKV 1155

Db 1038 NEDNETLAWEGVMKENYLKINTKANDTSEEMRHRFRQLDTKLNLDLKGLLKEIANKI 1094

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	7950	100.0	1503	1	TRL2_HUMAN	O94759 homo sapien
2	1282.5	16.1	2032	1	TRPG_CAEL	Q93971 caenorhabdi
3	659	8.3	1017	1	TRL3_HUMAN	Q9hcf6 homo sapien
4	450	5.7	1418	1	CE11_CAEL	P34641 caenorhabdi
5	436.5	5.5	350	1	NUD9_HUMAN	Q9bw91 homo sapien

6	377.5	4.7	260	1	YQ08_CAEEL	Q09297	caenorhabdi
7	356	4.5	1027	1	TRPL_CAEEL	P34586	caenorhabdi
8	344	4.3	1124	1	TRPL_DROME	P48994	drosophila
9	341.5	4.3	975	1	TRP5_MOUSE	Q9qx29	mus musculu
10	340	4.3	973	1	TRP5_HUMAN	Q9ul62	homo sapien
11	334.5	4.2	974	1	TRP5_RABIT	O62852	oryctolagus
12	331	4.2	885	1	TRP2_RAT	Q9r283	rattus norv
13	331	4.2	977	1	TRP4_HUMAN	Q9ubn4	homo sapien
14	324.5	4.1	981	1	TRP4_BOVIN	P79100	bos taurus
15	321.5	4.0	1275	1	TRP_DROME	P19334	drosophila
16	321	4.0	977	1	TRP4_RAT	O35119	rattus norv

RESULT 1

TRL2_HUMAN

ID TRL2_HUMAN STANDARD; PRT; 1503 AA.

AC O94759; Q96KN6;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Long transient receptor potential channel 2 (LTrpC2) (Transient receptor potential channel 7) (TrpC7).

GN TRPM2 OR LTRPC2 OR TRPC7 OR KNP3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=99026133; PubMed=9806837;

RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F., Shimizu N.;

RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7) highly expressed in brain.";

RL Genomics 54:124-131(1998).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=22075135; PubMed=11960981;

RA Wehage E., Eisfeld J., Heiner I., Jungling E., Zitt C., Luckhoff A.;

RT "Activation of the cation channel long transient receptor potential channel 2 (LTRPC2) by hydrogen peroxide. A splice variant reveals a mode of activation independent of ADP-ribose.";

RL J. Biol. Chem. 277:23150-23156(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20289799; PubMed=10830953;

RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.;

RT "The DNA sequence of human chromosome 21.";

RL Nature 405:311-319(2000).

CC -!- FUNCTION: May be a calcium channel.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=1;

CC IsoId=O94759-1; Sequence=Displayed;

CC Name=2;

CC IsoId=O94759-2; Sequence=VSP_006574, VSP_006575;

CC -!- TISSUE SPECIFICITY: Highly expressed in brain.

```

CC      -!- SIMILARITY: Belongs to the transient receptor family. LTrpC
CC      subfamily.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB001535; BAA34700.1; -.
DR      EMBL; AJ417076; CAD01139.1; -.
DR      EMBL; AP001754; BAA95563.1; -.
DR      Genew; HGNC:12339; TRPM2.
DR      MIM; 603749; -.
DR      GO; GO:0005887; C:integral to plasma membrane; TAS.
DR      GO; GO:0005262; F:calcium channel activity; TAS.
DR      GO; GO:0006816; P:calcium ion transport; TAS.
DR      InterPro; IPR002111; Cat_channel_TrpL.
DR      InterPro; IPR005821; Ion_trans.
DR      InterPro; IPR002153; Trans_receptor.
DR      Pfam; PF00520; ion_trans; 1.
DR      PRINTS; PR01097; TRNSRECEPTRP.
KW      Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW      Alternative splicing.
FT      DOMAIN      1      752      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      753      773      POTENTIAL.
FT      DOMAIN      774      795      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      796      816      POTENTIAL.
FT      DOMAIN      817      820      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      821      841      POTENTIAL.
FT      DOMAIN      842      896      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      897      917      POTENTIAL.
FT      DOMAIN      918      936      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      937      957      POTENTIAL.
FT      DOMAIN      958      1025     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM     1026      1046     POTENTIAL.
FT      DOMAIN      1047      1503     CYTOPLASMIC (POTENTIAL).
FT      VARSPLIC      538      557      Missing (in isoform 2).
FT                                          /FTId=VSP_006574.
FT      VARSPLIC     1291      1325     DTLEPLSTIQYNVVDGLRDRRSFHGPPYTVQAGLPL -> E
FT                                          (in isoform 2).
FT                                          /FTId=VSP_006575.
FT      CONFLICT     1088      1088      S -> N (IN REF. 2).
FT      CONFLICT     1189      1189      R -> Q (IN REF. 3).
SQ      SEQUENCE     1503 AA; 171225 MW; AD329AE79F1A71B5 CRC64;

Query Match      100.0%; Score 7950; DB 1; Length 1503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MEPSALRKAGSEQEEGFEGLP RRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60
      |||
Db      1  MEPSALRKAGSEQEEGFEGLP RRVTDLGMVSNLRRSNSSLFKSWRLQCPFGNNDKQESLS 60

Qy      61  SWIPENIKKKECVYFVSSKLS DAGKVVQC GYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120
      |||
Db      61  SWIPENIKKKECVYFVSSKLS DAGKVVQC GYTHEQHLEEATKPHTFQGTQWDPKKHVQ 120

Qy      121  EMPTDAFGDIVFTGLSQVKKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180
      |||
Db      121  EMPTDAFGDIVFTGLSQVKKKYVRVSQDTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNF 180

Qy      181  NMKPRKLSIFRRGLVKVAQT TGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240
      |||
Db      181  NMKPRKLSIFRRGLVKVAQT TGAWIITGGSHTGVMKQVGEAVRDFSLSSSYKEGELITIG 240

Qy      241  VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGV EIP 300
      |||
Db      241  VATWGTVHRREGLIHPTGSFPAEYILDEDGQGNLTCLDSNHSHFILVDDGTHGQYGV EIP 300

```

Qy	301	LRTRLEKFISEQTKERGGVAIKIPIVCVVLGGPGTLHTIDNATTNGTPCVVVEGSGRVA	360
Db	301	LRTRLEKFISEQTKERGGVAIKIPIVCVVLGGPGTLHTIDNATTNGTPCVVVEGSGRVA	360
Qy	361	DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR	420
Db	361	DVIAQVANLPVSDITISLIQQKLSVFFQEMFETFTESRIVEWTKKIQDIVRRRQLLTVFR	420
Qy	421	EGKDGQQDQVDVAILQALLKASRSQDHFHGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK	480
Db	421	EGKDGQQDQVDVAILQALLKASRSQDHFHGHENWDHQLKLAVAWNRVDIARSEIFMDEWQWK	480
Qy	481	PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL	540
Db	481	PSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYLYENLDPSCLFHSKLQKVL	540
Qy	541	VEDPERPACAPAAPRLQMHHVAQVLRRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLVNQ	600
Db	541	VEDPERPACAPAAPRLQMHHVAQVLRRELLGDFTQPLYPRPRHNDRLRLLLPVPHVKLVNQ	600
Qy	601	GVSLRSLYKRSSGHVFTFMDPIRDLLIWAIVQNRRELAGIWAQSQDCIAAALACSKILK	660
Db	601	GVSLRSLYKRSSGHVFTFMDPIRDLLIWAIVQNRRELAGIWAQSQDCIAAALACSKILK	660
Qy	661	ELSKEEEDTDSSEMLALAEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL	720
Db	661	ELSKEEEDTDSSEMLALAEYEHRAIGVFTECYRKDEERAQKLLTRVSEAWGKTTCLQL	720
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SEQ ID NO: 2

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7	4163.2	92.3	5284	9	HSA417076	AJ417076 Homo sapi
8	3220	71.4	5980	10	MMU344343	AJ344343 Mus muscu
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RESULT 4

AX042216

LOCUS AX042216 6220 bp DNA linear PAT 23-NOV-2000

DEFINITION Sequence 5 from Patent WO0065056.

ACCESSION AX042216

VERSION AX042216.1 GI:11340930

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Scharenberg, A.M.

TITLE Nucleic acids encoding a mutt domain-containing polypeptide

JOURNAL Patent: WO 0065056-A 5 02-NOV-2000; Beth Israel Deaconess Medical Center, Inc. (US)

FEATURES

source

Location/Qualifiers

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RESULT 6

AB001535

LOCUS AB001535 6220 bp mRNA linear PRI 28-NOV-1998
 DEFINITION Homo sapiens mRNA, complete cds.
 ACCESSION AB001535
 VERSION AB001535.1 GI:3928755
 KEYWORDS KNP3.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Nagamine,K., Kudoh,J., Minoshima,S., Kawasaki,K., Asakawa,S.,
 Ito,F. and Shimizu,N.
 TITLE Molecular cloning of a novel putative Ca²⁺ channel protein (TRPC7)
 highly expressed in brain
 JOURNAL Genomics 54 (1), 124-131 (1998)
 MEDLINE 99026133
 PUBMED 9806837
 REFERENCE 2 (bases 1 to 6220)
 AUTHORS Shimizu,N.

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SUMMARIES

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		Match	Length			
1	4512	100.0	6220	4	US-09-600-087-1	Sequence 1, Appli
2	611.6	13.6	3639	4	US-09-636-215-779	Sequence 779, App
3	611.6	13.6	3639	4	US-09-685-166A-779	Sequence 779, App
4	607.2	13.5	5668	3	US-09-112-096-14	Sequence 14, Appl
5	607.2	13.5	5668	4	US-09-636-215-777	Sequence 777, App
6	607.2	13.5	5668	4	US-09-685-166A-777	Sequence 777, App
7	379.8	8.4	3848	3	US-09-112-096-28	Sequence 28, Appl
8	306	6.8	1959	4	US-09-636-215-817	Sequence 817, App
9	306	6.8	1959	4	US-09-685-166A-817	Sequence 817, App
10	302.8	6.7	1690	3	US-09-112-096-27	Sequence 27, Appl
11	250.2	5.5	1512	4	US-09-461-325-54	Sequence 54, Appl
12	250.2	5.5	1512	4	US-10-012-542-54	Sequence 54, Appl
13	244.8	5.4	1524	3	US-09-020-956-109	Sequence 109, App
14	244.8	5.4	1524	3	US-09-030-607-109	Sequence 109, App
15	244.8	5.4	1524	4	US-09-439-313-109	Sequence 109, App
16	244.8	5.4	1524	4	US-09-352-616A-109	Sequence 109, App

RESULT 1

US-09-600-087-1

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; Sequence 1, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6548272uyoshi
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
; FILE REFERENCE: 11283-004001
; CURRENT APPLICATION NUMBER: US/09/600,087
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: PCT/JP99/06289
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JP/321200/1998
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (446)...(4954)
; NAME/KEY: polyA_signal
; LOCATION: (5812)...(5817)
US-09-600-087-1

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Query Match      100.0%; Score 4512; DB 4; Length 6220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2041 GAGTATGAGCACAGAGCCATCGGGGTCTTACCAGAGTGCTACCGGAAGGACGAAGAGAGA 2100
 |||
 Db 2486 GAGTATGAGCACAGAGCCATCGGGGTCTTACCAGAGTGCTACCGGAAGGACGAAGAGAGA 2545
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QY 2101 GCCCAGAACTGCTCACCCGCGTGTCCGAGGCTGGGGGAAGACCCTGCCTGCAGCTC 2160
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 Db 2546 GCCCAGAACTGCTCACCCGCGTGTCCGAGGCTGGGGGAAGACCCTGCCTGCAGCTC 2605
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QY 2161 GCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTACGGGGCATCCAGGCCTTCTGACC 2220
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Db 2606 GCCCTGGAGGCCAAGGACATGAAGTTTGTGTCTCACGGGGGCATCCAGGCCTTCCTGACC 2665
 QY 2221 AAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGGGCTGTGGCGTGTGACCCTGTGCATG 2280
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 Db 2666 AAGGTGTGGTGGGGCCAGCTCTCCGTGGACAATGGGCTGTGGCGTGTGACCCTGTGCATG 2725
 QY 2281 CTGGCCTTCCCCTGCTCCTCACCGGCTCATCTCCTTCAGGGAGAAGAGGCTGCAGGAT 2340
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 Db 2726 CTGGCCTTCCCCTGCTCCTCACCGGCTCATCTCCTTCAGGGAGAAGAGGCTGCAGGAT 2785
 QY 2341 GTGGGCACCCCCGCGGCCCGCGCCCGTGCCTTCTTCACCGCACCCGTGGTGGTCTTCCAC 2400
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 Db 2786 GTGGGCACCCCCGCGGCCCGCGCCCGTGCCTTCTTCACCGCACCCGTGGTGGTCTTCCAC 2845
 QY 2401 CTGAACATCCTCTCCTACTTCGCCTTCTCTGCTGTTCGCCTACGTGCTCATGGTGGAC 2460
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 Db 2846 CTGAACATCCTCTCCTACTTCGCCTTCTCTGCTGTTCGCCTACGTGCTCATGGTGGAC 2905
 QY 2461 TTCCAGCCTGTGCCCTCCTGGTGCGAGTGTGCCATCTACCTCTGGCTCTTCTCCTTGGTG 2520
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 Db 2906 TTCCAGCCTGTGCCCTCCTGGTGCGAGTGTGCCATCTACCTCTGGCTCTTCTCCTTGGTG 2965
 QY 2521 TGCGAGGAGATGCGGCAGCTCTTCTATGACCCTGACGAGTGCGGGCTGATGAAGAAGGCA 2580
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 Db 2966 TGCGAGGAGATGCGGCAGCTCTTCTATGACCCTGACGAGTGCGGGCTGATGAAGAAGGCA 3025
 QY 2581 GCCTTGTACTTCAGTGACTTCTGGAATAAGCTGGACGTGCGCGCAATCTTGCTCTTCGTG 2640
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 Db 3026 GCCTTGTACTTCAGTGACTTCTGGAATAAGCTGGACGTGCGCGCAATCTTGCTCTTCGTG 3085
 QY 2641 GCAGGGCTGACCTGCAGGCTCATCCCGGCGACGCTGTACCCCGGGCGCGTATCCTCTCT 2700
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 Db 3086 GCAGGGCTGACCTGCAGGCTCATCCCGGCGACGCTGTACCCCGGGCGCGTATCCTCTCT 3145
 QY 2701 CTGGACTTCATCCTGTTCTGCCTCCGGCTCATGCACATTTTACCATCAGTAAGACGCTG 2760
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 QY 2761 GGGCCCAAGATCATCATTGTGAAGCGGATGATGAAGGACGTCTTCTTCTCCTCTTCCTG 2820
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 QY 2821 CTGGCTGTGTGGGTGGTGTCTTCCGGGTGGCCAAGCAGGCCATCCTCATCCACAACGAG 2880
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 Db 3266 CTGGCTGTGTGGGTGGTGTCTTCCGGGTGGCCAAGCAGGCCATCCTCATCCACAACGAG 3325
 QY 2881 CGCCGGGTGGACTGGCTGTTCCGAGGGGCGTCTACCACTCCTACCTCACCATCTTCGGG 2940
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 Db 3326 CGCCGGGTGGACTGGCTGTTCCGAGGGGCGTCTACCACTCCTACCTCACCATCTTCGGG 3385
 QY 2941 CAGATCCCGGGCTACATCGACGGTGTGAACTTCAACCCGGAGCACTGCAGCCCCAATGGC 3000
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 Db 3386 CAGATCCCGGGCTACATCGACGGTGTGAACTTCAACCCGGAGCACTGCAGCCCCAATGGC 3445
 QY 3001 ACCGACCCCTACAAGCCTAAGTGCCCCGAGAGCGACGCGACGAGAGGCGCGCCTTC 3060
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 Db 3446 ACCGACCCCTACAAGCCTAAGTGCCCCGAGAGCGACGCGACGAGAGGCGCGCCTTC 3505
 QY 3061 CCTGAGTGGCTGACGGTCTCCTACTCTGCCTTACCTGCTCTTACCAACATCCTGCTG 3120
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 Db 3506 CCTGAGTGGCTGACGGTCTCCTACTCTGCCTTACCTGCTCTTACCAACATCCTGCTG 3565
 QY 3121 CTCAACCTCCTCATCGCCATGTTCAACTACACCTTCCAGCAGGTGCAGGAGCACACGGAC 3180
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 Db 3566 CTCAACCTCCTCATCGCCATGTTCAACTACACCTTCCAGCAGGTGCAGGAGCACACGGAC 3625
 QY 3181 CAGATTGGAAGTTCCAGCGCCATGACCTGATCGAGGAGTACCACGGCCGCCCCGCGCG 3240
 |||||
 Db 3626 CAGATTGGAAGTTCCAGCGCCATGACCTGATCGAGGAGTACCACGGCCGCCCCGCGCG 3685
 QY 3241 CCGCCCCCTTATCCTCCTCAGCCACCTGCAGCTCTTATCAAGAGGGTGGTCTGAAG 3300

Db	3686		CCGCCCCCTTCATCCTCCTCAGCCACCTGCAGCTCTTCATCAAGAGGGTGGTCCTGAAG	3745
QY	3301		ACTCCGGCCAAGAGGCACAAGCAGCTCAAGAACAAGCTGGAGAAGAACGAGGAGCGGCC	3360
Db	3746		ACTCCGGCCAAGAGGCACAAGCAGCTCAAGAACAAGCTGGAGAAGAACGAGGAGCGGCC	3805
QY	3361		CTGCTATCCTGGGAGATCTACCTGAAGGAGAACTACCTCCAGAACCGACAGTTCCAGCAA	3420
Db	3806		CTGCTATCCTGGGAGATCTACCTGAAGGAGAACTACCTCCAGAACCGACAGTTCCAGCAA	3865
QY	3421		AAGCAGCGGCCCCGAGCAGAAGATCGAGGACATCAGCAATAAGGTTGACGCCATGGTGGAC	3480
Db	3866		AAGCAGCGGCCCCGAGCAGAAGATCGAGGACATCAGCAATAAGGTTGACGCCATGGTGGAC	3925
QY	3481		CTGCTGGACCTGGACCCACTGAAGAGGTGCGGCTCCATGGAGCAGAGGTTGGCCTCCCTG	3540
Db	3926		CTGCTGGACCTGGACCCACTGAAGAGGTGCGGCTCCATGGAGCAGAGGTTGGCCTCCCTG	3985
QY	3541		GAGGAGCAGGTGGCCCAGACAGCCCGAGCCCTGCACTGGATCGTGAGGACGCTGCGGGCC	3600
Db	3986		GAGGAGCAGGTGGCCCAGACAGCCCGAGCCCTGCACTGGATCGTGAGGACGCTGCGGGCC	4045
QY	3601		AGCGGCTTCAGCTCGGAGGCGGACGTCCCACTCTGGCCTCCAGAAGGCCGCGGAGGAG	3660
Db	4046		AGCGGCTTCAGCTCGGAGGCGGACGTCCCACTCTGGCCTCCAGAAGGCCGCGGAGGAG	4105
QY	3661		CCGGATGCTGAGCCGGGAGGAGGAGGAAGAAGACGGAGGAGCCGGGCGACAGTACCACGTG	3720
Db	4106		CCGGATGCTGAGCCGGGAGGAGGAGGAAGAAGACGGAGGAGCCGGGCGACAGTACCACGTG	4165
QY	3721		AATGCCCGGCACCTCCTCTACCCCAACTGCCCTGTACGCGCTTCCCCGTGCCCAACGAG	3780
Db	4166		AATGCCCGGCACCTCCTCTACCCCAACTGCCCTGTACGCGCTTCCCCGTGCCCAACGAG	4225
QY	3781		AAGGTGCCCTGGGAGACGGAGTTCTTGATCTATGACCCACCCTTTTACACGGCAGAGAGG	3840
Db	4226		AAGGTGCCCTGGGAGACGGAGTTCTTGATCTATGACCCACCCTTTTACACGGCAGAGAGG	4285
QY	3841		AAGGACGCGCGCCCATGGACCCCATGGGAGACACCCTGGAGCCACTGTCCACGATCCAG	3900
Db	4286		AAGGACGCGCGCCCATGGACCCCATGGGAGACACCCTGGAGCCACTGTCCACGATCCAG	4345
QY	3901		TACAACGTGGTGGATGGCCTGAGGGACCGCGGAGCTTCCACGGGCCGTACACAGTGCAG	3960
Db	4346		TACAACGTGGTGGATGGCCTGAGGGACCGCGGAGCTTCCACGGGCCGTACACAGTGCAG	4405
QY	3961		GCCGGGTTGCCCCGAACCCCATGGGCCGCACAGGACTGCGTGGGCGCGGGAGCCTCAGC	4020
Db	4406		GCCGGGTTGCCCCGAACCCCATGGGCCGCACAGGACTGCGTGGGCGCGGGAGCCTCAGC	4465
QY	4021		TGCTTCGGACCCAACACACGCTGTACCCCATGGTCACGCGGTGGAGGCGGAACGAGGAT	4080
Db	4466		TGCTTCGGACCCAACACACGCTGTACCCCATGGTCACGCGGTGGAGGCGGAACGAGGAT	4525
QY	4081		GGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCTGGAAGTGCTGGTGGTGAAGCTCCCT	4140
Db	4526		GGAGCCATCTGCAGGAAGAGCATAAAGAAGATGCTGGAAGTGCTGGTGGTGAAGCTCCCT	4585
QY	4141		CTCTCCGAGCACTGGGCCCTGCCTGGGGGCTCCCGGAGCCAGGGGAGATGCTACCTCGG	4200
Db	4586		CTCTCCGAGCACTGGGCCCTGCCTGGGGGCTCCCGGAGCCAGGGGAGATGCTACCTCGG	4645
QY	4201		AAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCCGTCTTTTGAAAACCTTGCTGAAGTGC	4260
Db	4646		AAGCTGAAGCGGATCCTCCGGCAGGAGCACTGGCCGTCTTTTGAAAACCTTGCTGAAGTGC	4705
QY	4261		GGCATGGAGGTGTACAAAGGCTACATGGATGACCCGAGGAACACGGACAATGCCTGGATC	4320
Db	4706		GGCATGGAGGTGTACAAAGGCTACATGGATGACCCGAGGAACACGGACAATGCCTGGATC	4765

Qy	4321	GAGACGGTGGCCGTCAGCGTCCACTTCCAGGACCAGAATGACGTGGAGCTGAACAGGCTG	4380
Db	4766	GAGACGGTGGCCGTCAGCGTCCACTTCCAGGACCAGAATGACGTGGAGCTGAACAGGCTG	4825
Qy	4381	AACTCTAACCTGCACGCCCTGCGACTCGGGGGCCTCCATCCGATGGCAGGTGGTGGACAGG	4440
Db	4826	AACTCTAACCTGCACGCCCTGCGACTCGGGGGCCTCCATCCGATGGCAGGTGGTGGACAGG	4885
Qy	4441	CGCATCCCCTCTATGCGAACCACAAGACCTCTCTCCAGAAGGCAGCCGCTGAGTTCCGGG	4500
Db	4886	CGCATCCCCTCTATGCGAACCACAAGACCTCTCTCCAGAAGGCAGCCGCTGAGTTCCGGG	4945
Qy	4501	GCTCACTACTGA	4512
Db	4946	GCTCACTACTGA	4957

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L3 3 LTRPC2 (S) SCREEN?

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

=> d l4 total ibib

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:320077 CAPLUS
DOCUMENT NUMBER: 138:331656
TITLE: Method for screening cell death inhibitor
INVENTOR(S): Sano, Yorikata; Inamura, Kohei; Miyake, Akira; Yokoi,
Hiromichi; Nozawa, Katsura; Mochizuki, Shinobu
PATENT ASSIGNEE(S): Yamanouchi Pharmaceutical Co., Ltd., Japan
SOURCE: PCT Int. Appl., 98 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003033727	A1	20030424	WO 2002-JP8128	20020808
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.: JP 2001-315339 A 20011012
JP 2002-21175 A 20020130
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:575231 CAPLUS
DOCUMENT NUMBER: 137:119632
TITLE: Screening for modulators of human Ca²⁺-ATP regulated long transient receptor potential channel (LTRPC7)
INVENTOR(S): Penner, Reinhold; Fleig, Andrea
PATENT ASSIGNEE(S): The Queen's Medical Center, USA

SOURCE: PCT Int. Appl., 80 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002059307	A2	20020801	WO 2001-US47784	20011113
WO 2002059307	A3	20030605		
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
EP 1337635	A2	20030827	EP 2001-270129	20011113
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
PRIORITY APPLN. INFO.:			US 2000-248235P	P 20001113
			US 2000-254468P	P 20001208
			WO 2001-US47784	W 20011113

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:368512 CAPLUS

DOCUMENT NUMBER: 136:363809

TITLE: Protein and cDNA sequences of a novel human long transient receptor potential channel (**LTRPC2**) and methods of **screening** for its modulators

INVENTOR(S): Penner, Reinhold; Fleig, Andrea

PATENT ASSIGNEE(S): The Queen's Medical Center, USA

SOURCE: PCT Int. Appl., 60 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002038608	A2	20020516	WO 2001-US47331	20011113
WO 2002038608	A3	20030313		
WO 2002038608	C2	20030530		
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
AU 2002028903	A5	20020521	AU 2002-28903	20011113
US 2002182635	A1	20021205	US 2001-7706	20011113
EP 1334129	A2	20030813	EP 2001-990026	20011113
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
PRIORITY APPLN. INFO.:			US 2000-248442P	P 20001113
			US 2000-254528P	P 20001208
			WO 2001-US47331	W 20011113